AMENDMENT TO SPECIFICATION

Please replace lines 1-20 on page 12 with the following amended paragraph:

Characterization can include determination of whether the transposon has been incorporated into the genome. This can be accomplished using well known techniques such as Southern blotting, dot or slot blots, and in situ hybridization to bacterial chromosomes, using a polynucleotide probe complimentary to the transposon used. Information regarding the location of the transposition and the gene or sequence disrupted can be obtained by sequencing. In general, this can be accomplished by obtaining purified genomic DNA from transfected bacteria and cutting DNA with restriction enzymes that do not cut within the transposon. The restriction fragments obtained can be cloned into a cloning vector using standard techniques and amplified for sequencing. Any known method of sequencing can be used. In one embodiment, sequencing is accomplished by cycle sequencing outward from the transposon. Once the sequence information has been obtained, the nucleic acid sequences or deduced amino acid sequences can be compared to sequences in ~~publically~~ publicly available databases such as those maintained by the National Center for Biotechnology Information ~~at http://www.nebi.nlm.nih.gov/~~ (National Library of Medicine; National Institute of Health), the European Bioinformatics Institute ~~at http://www.ebi.ac.uk/~~ (European Molecular Biology Laboratory), The Institute for Genomic Research ~~at http://www.tigr.org~~ (TIGR), The Sanger Centre ~~at http://www.sanger.ac.uk/Projects/~~, The Computational Biology Center of the University of Minnesota Microbial Genome Project ~~at htt://www.cbc.umn.edu/~~, and the Institute Pasteur ~~at http://genolist.pasteur.fr/~~ all of which are incorporated herein by reference. Based on sequence homology, the identity of the gene or sequence disrupted by the insertion can be determined and thus the virulence determinant identified.